

SEQUENCE LISTING

<110> SALONEN, Jukka T.
 PIRSKANEN, Mia
 TUOMAINEN, Tomi-Pekka
 YUNUS, Faisel

<120> METHOD AND KIT FOR DETECTING A RISK OF DIABETES OR A METABOLIC SYNDROME

<130> 0933-0247PUS1

<140> US 10/538,198
 <141> 2005-06-09

<150> PCT/FI03/00946
 <151> 2003-12-11

<150> FI 20022178
 <151> 2002-12-11

<160> 6

<170> PatentIn version 3.1

<210> 1
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1341)
 <223> ADRA2B variant type sequence

<400> 1

atg gac cac cag gac ccc tac tcc gtg cag gcc aca gcg gcc ata gcg	48
Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala	
1 5 10 15	
gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg	96
Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu	
20 25 30	
gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac	144
Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn	
35 40 45	
ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc	192
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu	
50 55 60	
atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc	240
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe	
65 70 75 80	
cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc	288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys	

85	90	95	
acc tgc tcc atc gtg cac. ctg tgc gcc atc agc ctg gac cgc tac tgg			336
Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp			
100	105	110	
gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc			384
Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg			
115	120	125	
atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tgc			432
Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser			
130	135	140	
ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg			480
Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly			
145	150	155	160
cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc			528
Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser			
165	170	175	
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac			576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr			
180	185	190	
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg			624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg			
195	200	205	
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac			672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp			
210	215	220	
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg			720
His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val			
225	230	235	240
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag			768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys			
245	250	255	
gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc			816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro			
260	265	270	
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt			864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val			
275	280	285	
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag			912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu			
290	295	300	
gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc			960
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys			
305	310	315	320

agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg gcc acc cta 1008
 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
 325 330 335
 cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag 1056
 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
 340 345 350
 tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc ttc acc ttc 1104
 Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
 355 360 365
 gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc 1152
 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
 370 375 380
 ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg 1200
 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
 385 390 395 400
 ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc 1248
 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
 405 410 415
 tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt 1296
 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
 420 425 430
 gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga 1344
 Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
 435 440 445

<210> 2
 <211> 447
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15
 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
 20 25 30
 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45
 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
 115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
 130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
 145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
 165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
 180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
 195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
 210 215 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
 225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
 245 250 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
 260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
 275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu

290	295	300
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys		
305	310	315 320
Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu		
	325	330 335
Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln		
	340	345 350
Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe		
	355	360 365
Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe		
	370	375 380
Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val		
385	390	395 400
Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser		
	405	410 415
Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg		
	420	425 430
Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp		
	435	440 445

<210> 3
 <211> 1353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1350)
 <223> ADRA2B wild type sequence

<400> 3	
atg gac cac cag gac ccc tac tcc gtg cag gcc aca gcg gcc ata gcg	48
Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala	
1 5 10 15	
gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg	96
Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu	
20 25 30	

gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn 35 40 45	144
ctg ttc ctg gtg tgc ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu 50 55 60	192
atc atc cct ttc tgc ctg gcc aac gag ctg ctg ggc tac tgg tac ttc Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe 65 70 75 80	240
cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys 85 90 95	288
acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp 100 105 110	336
gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg 115 120 125	384
atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser 130 135 140	432
ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly 145 150 155 160	480
cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser 165 170 175	528
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr 180 185 190	576
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg 195 200 205	624
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp 210 215 220	672
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val 225 230 235 240	720
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys 245 250 255	768

gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro 260 265 270	816
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val 275 280 285	864
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu 290 295 300	912
gag gag gag gaa gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala 305 310 315 320	960
tca gct tgc agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu 325 330 335	1008
gcc acc cta cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile 340 345 350	1056
ggg ggg cag tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc Gly Gly Gln Trp Trp Arg Arg Ala His Val Thr Arg Glu Lys Arg 355 360 365	1104
ttc acc ttc gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp 370 375 380	1152
ttc ccc ttc ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His 385 390 395 400	1200
tgc aag gtg ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr 405 410 415	1248
tgc aac agc tca ctg aac cct gtt atc tac acc atc ttc aac cag gac Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp 420 425 430	1296
ttc cgc cgt gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr 435 440 445	1344
gcc tgg tga Ala Trp 450	1353

<210> 4
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
1 5 10 15

Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
20 25 30

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
210 215 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
 225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
 245 250 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
 260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
 275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
 290 295 300

Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
 305 310 315 320

Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
 325 330 335

Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
 340 345 350

Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg
 355 360 365

Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
 370 375 380

Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
 385 390 395 400

Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
 405 410 415

Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
 420 425 430

Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr
 435 440 445

Ala Trp
450

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> ADRA2B pcr primer f

<400> 5
gggtgtttgt ggggcatctc 20

<210> 6
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> ADRA2B pcr primer r

<400> 6
tggcactgcc tggggttca 19